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METHODS FOR MEASURING RATES OF REVERSE CHOLESTEROL TRANSPORT IN VIVO, AS AN INDEX OF ANTI-ATHEROGENESIS

PRIORITY CLAIM

This application claims priority to 60/410,352 filed on September 13, 2002, which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates to the field of cholesterol metabolism. In particular, methods for quantitatively measuring reverse cholesterol transport are described.

BACKGROUND OF THE INVENTION

Atherosclerosis, the most common form of arteriosclerosis, is a disease of large and medium-sized arteries (e.g., coronary, carotid, and lower extremity arteries), and of the elastic arteries, such as the aorta and iliac vessels. The atheroma, or fibrofatty plaque within the intima that consists of a lipid core and fibrous cap, is pathognomonic (*Robbins Pathologic Basis of Disease* 557 (Cotran et al. eds., 4th ed. 1989)). In addition to being a primary risk factor for myocardial and cerebral infarcts, atherosclerosis is responsible for such medical conditions as chronic lower extremity ischemia and gangrene, and for mesenteric occlusion. Despite a recent reduction in mortality from coronary heart disease, about 50% of all deaths in the United States are still attributed to atherosclerosis (*Scientific American Medicine* §1 (Rubenstein et al. eds., 1991)).

Epidemiologic, postmortem, and angiographic studies have firmly established a causal relationship between elevated serum cholesterol levels and the genesis of atherosclerosis (Levine et al., *Cholesterol Reduction In Cardiovascular Disease*, N Eng J Med 332(8):512-521 (1995)). Although there is no single level of plasma cholesterol that identifies those at risk, in general, the higher the level, the higher the risk. However, the risk rises significantly with cholesterol levels above 200 mg/dl (*Robbins Pathologic Basis of Disease*, supra, at 559). Levels of total cholesterol are typically classified as being desirable (<200 mg/dl), borderline high (200-239 mg/dl), or high (≥240 mg/dl). Dietary treatment is usually recommended for patients with high

risk levels of low density lipoprotein (LDL) cholesterol and for those with borderline-high risk levels who have at least 2 additional risk factors for atherosclerosis (e.g., hypertension, diabetes mellitus, cigarette smoking, etc.). However, dietary therapy has been found to be effective only in patients whose diets were higher than average in cholesterol and saturated fats (*Adult Treatment Panel II. National Cholesterol Education Program: Second Report of the Expert Panel on Detection, Evaluation, and Treatment of High Blood Cholesterol in Adults*, Circulation 89:1333-1445 (1994)), and would be ineffective in patients with a genetic predisposition to hypercholesterolemia. In the case of persistent high cholesterol levels, drug therapy may be prescribed.

Currently marketed drugs for the treatment of hypercholesterolemia work by such methods as inhibiting *de novo* cholesterol synthesis and/or stimulating clearance of LDL cholesterol by the LDL receptor (e.g., lovastatin), decreasing the production of very low density lipoprotein (VLDL) (e.g., gemfibrozil), or by inhibiting bile acid reabsorption in the intestines (e.g., cholestyramine). Examination of cholesterol metabolism, however, also reveals that the process of reverse cholesterol transport allows a pathway through which cholesterol may be removed from tissues and may exit the body. At present, there is no known method for measuring the rate of cholesterol flow through the reverse cholesterol transport pathway from tissue to excretion in a living organism.

Reverse cholesterol transport (RCT) is a biological pathway through which cholesterol is mobilized and transported from the peripheral tissues of the body to the liver. As shown in Figure 1, there are two arms of the pathway, represented by efflux of cholesterol from extrahepatic tissues (the high density lipoprotein (HDL) arm or first arm of RCT) and transport of cholesterol from the bloodstream to the liver (post-HDL arm or second arm of RCT). Eventually, cholesterol is excreted into the bile, and then ultimately, from the body. RCT represents the only known biological pathway or active mechanism by which cholesterol can be removed from tissues. As mentioned above, because of the well-established role of cholesterol in atherogenesis, RCT is considered a key anti-atherogenic process and is generally believed to be the explanation for anti-atherogenic properties and clinical correlation with reduced cardiovascular risk of the high density lipoprotein (HDL) fraction of plasma.

However, HDL levels are now recognized to reflect only one component of the molecular pathway of RCT (Figure 1), and do not necessarily reflect the true flow of cholesterol through

the RCT pathway. The RCT pathway involves the transport of cholesterol from extrahepatic tissues into plasma by HDL, then delivery to IDL (intermediate density lipoprotein) via the action of lecithin-cholesterol acyl transferase (LCAT), and then eventually to LDL (low density lipoprotein). Thereafter, some of the LDL is taken up by the liver and excreted as bile acids into the intestines (Ganong W.F., *Review of Medical Physiology* 284-288 (15th ed. 1991)). Other pathways of RCT have been considered but the above-noted sequence is currently believed to most likely predominate.

The molecular details of the RCT pathway have come into increasing focus in the past several years. One important implication of these recent advances in molecular understanding is the recognition that plasma HDLc (HDL-cholesterol) levels in isolation may or may not reflect true flux through the pathway, depending upon the underlying mechanism responsible for the change in HDLc. For example, if the plasma concentration of HDLc in an individual represents flux from tissues through ABC(A)-1 (the ATP-binding cassette transporter) into plasma apoAI-containing particles, as in ABC(A)-I heterozygotes, then HDLc is a useful marker. However, if HDLc in another individual accumulates because of inhibition of delivery of HDLc to its acceptors (e.g., due to reduced cholesterol ester transfer protein activity, reduced hepatic SRBI (scavenger-receptor BI) activity), then HDLc levels will not reflect RCT. The situation can be particularly complex, when considering the impact on RCT of interventions that alter the production and fate of apoB containing particles, such as the statins. Because apoB particles are capable of carrying cholesterol forward (i.e., to the tissues) as well as in reverse (i.e., back to the liver), the actual fate of apoB particles in an individual may contribute to the efficiency of RCT at any plasma HDL level. The possibility of a dissociation between HDLc concentrations and RCT is thereby raised in the setting of effective statin therapy (or any other intervention that promotes return of VLDL and LDL particles to the liver).

Measuring the rate of a biochemical process such as RCT is more difficult than measuring the concentration of biochemical molecules. The former requires kinetic methods, while the latter involves static measurements. Kinetic measurements must include the dimension of time (i.e., a timed procedure must be performed), because all rates include time in the denominator (e.g., mg/min for biochemical rates, analogous to miles/hour for physical rates of motion). Typically, for biochemical kinetics, the molecule of interest or a precursor to it is

labeled, and the flow of the label from the labeled molecule into various routes is measured over time.

Theoretically, tissue cholesterol may be labeled to follow its efflux from peripheral cells, but in practice, it has been essentially impossible to label non-hepatic cholesterol without labeling hepatic and blood cholesterol at the same time, whether the labeled material administered is cholesterol itself or its biosynthetic precursors (e.g., ^{14}C-acetate, $^{3}H_2O$, or $^{2}H_2O$). This is the case for several reasons: 1) hepatic cholesterol synthesis is very active, so that standard labeled biosynthetic precursors for cholesterol in the body will unavoidably label cholesterol in the liver; 2) there are no known labeled substrates that target peripheral (non-hepatic) tissues exclusively; 3) the cholesterol pools in peripheral tissues are very large and slow to turn over, so it takes a long time (weeks or months) to achieve adequate labeling; and 4) cholesterol exchanges rapidly between liver, blood and tissues, so that it quickly becomes impossible to distinguish the origin of labeled cholesterol and to infer directional rates of transfer.

For all these reasons, an *in vivo* method for measuring the rate of reverse cholesterol transport is needed and would have great utility for medical care and drug discovery and development.

SUMMARY OF THE INVENTION

To meet these needs, the present invention provides methods for determining the rate of reverse cholesterol transport. In one aspect, the first arm of reverse cholesterol transport may be determined in a living system. One or more isotopically labeled isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors are administered to the living system for a period of time sufficient for the label to be incorporated in plasma HDL. One or more isotopically labeled cholesterol molecules are obtained from plasma HDL. The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the cholesterol molecules is then measured. The rate of dilution of the isolated labeled cholesterol molecules by endogenous unlabeled cholesterol is then calculated to determine the rate of the first arm of reverse cholesterol transport in the living system.

In another aspect, the rate of the second arm of reverse cholesterol transport may be determined. First, the rate of the first arm of reverse cholesterol transport is determined as described above. One or more isotopically labeled bile acids are administered to the living system in a manner different than the manner in which the label of the isotopically labeled HDL particle, isotopically labeled cholesterol, or isotopically labeled cholesterol precursor molecule. Alternatively, the isotopically labeled bile acids are labeled with a different isotope than the isotopically labeled HDL particle, isotopically labeled cholesterol, or isotopically labeled cholesterol precursor molecule. One or more isotopically labeled bile acids are obtained from the living system. The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the bile acid is measured. The molecular flux rate of converting plasma HDL-cholesterol to bile acids is calculated to determine the rate of second arm of reverse cholesterol transport in the living system.

Suitable bile acids for labeling include, but are not limited to, cholic acid, chenodeoxycholic acid, deoxycholic acid, and lithocholic acid. Preferably, the bile acid is cholic acid.

Techniques for isotopically labeling molecules, e.g., cholesterol, bile acids, and the like, are well known in the art. The isotopes that may be used for labeling include, but are not limited to, ^{2}H, ^{3}H, ^{13}C, ^{14}C, or ^{18}O. The preferred cholesterol molecules for labeling are cholesterol esters.

Instead of being reconstituted *ex vivo*, in another variation, the HDL particles may be formed *in vivo*, by administering isotopically labeled cholesterol or an isotopically labeled cholesterol precursor to the subject, followed by isolation and purification of the labeled HDL from plasma and re-introduction to a different subject or to the same subject.

Furthermore, the methods of the present invention may be applied to assess the effect of drug agents on the risk for atherosclerosis. In general, the method involves administering the drug agent to a subject, comparing the rate of reverse cholesterol transport in the subject before and after administration of the drug agents or in comparison to matched subject who have not received the drug agents, and calculating the difference in the rate of reverse cholesterol transport before and after administration of the drug agent. The drug agent may be a known pharmaceutical agent or a known deoxyribonucleic acid molecule that affects atherosclerosis.

In another variation, the effect of dietary modification on the risk for atherosclerosis is assessed by comparing the rate of reverse cholesterol transport in the subject before and after dietary modification, and calculating the difference in the rate of reverse cholesterol transport before and after dietary modification.

In yet a further variation, kits for determining the rate of reverse cholesterol transport are provided. The kits may include labeled HDL particles, labeled cholesterol, labeled bile acids, or a combination thereof, and instructions for use of the kit. The kit may optionally also include tools for administration of labeled HDL particles, labeled cholesterol precursors, or labeled bile acids to the subject and instruments for collecting a sample from the subject.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates the reverse cholesterol transport pathway.

Figure 2 is a timeline that demonstrates a protocol for determining the rate of reverse cholesterol transport.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides a biochemical test for quantitatively measuring reverse cholesterol transport *in vivo* using isotopically labeled cholesterol and bile acids.

General Techniques

Practice of the present invention will generally utilize, unless otherwise indicated, conventional techniques of molecular biology, microbiology, cell biology, biochemistry, and immunology, which are within the skill of the art. Such techniques are fully explained in the literature, for example, in Cell Biology: A Laboratory Notebook (J.E. Cellis, ed., 1998); Current Protocols in Molecular Biology (F.M. Ausubel et al., eds, 1987); Short Protocols in Molecular Biology (Wiley and Sons, 1999); *Mass Isotopomer Distribution Analysis: A Technique for Measuring Biosynthesis and Turnover of Polymers* (Hellerstein et al., Am J Physiol 263 (Endocrinol Metab 26):E988-E1001 (1992)); and Mass Isotopomer Distribution Analysis at Eight Years: Theoretical, Analytic, and Experimental Considerations (Hellerstein et al., Am J Physiol 276 (Endocrinol Metab 39):E1146-1170 (1999)). Furthermore, procedures employing

commercially available assay kits and reagents will typically be used according to manufacturer defined protocols unless otherwise noted.

Definitions

By "living system" is meant herein any living entity including a cell, cell line, tissue, organ, and organism. Examples of organisms include any animal, preferably a vertebrate, more preferably a mammal, most preferably a human. Examples of mammals include nonhuman primates, farm animals, pet animals, for example cats and dogs, and research animals, for example mice, rats, and humans.

"Isotope labeled substrate" includes any isotope-labeled precursor molecule that is able to be incorporated into a molecule of interest in a living system. Examples of isotope labeled substrates include, but are not limited to, $^{2}H_2O$, $^{3}H_2O$, ^{2}H-glucose, ^{2}H-labeled amino acids, ^{2}H-labeled organic molecules, ^{13}C-labeled organic molecules, ^{14}C-labeled organic molecules, $^{13}CO_2$, $^{14}CO_2$, ^{15}N-labeled organic molecules and $^{15}NH_3$.

"Isotopologues" refer to isotopic homologues or molecular species that have identical elemental and chemical compositions but differ in isotopic content (e.g., CH_3NH_2 vs. CH_3NHD in the example above). Isotopologues are defined by their isotopic composition, therefore each isotopologue has a unique exact mass but may not have a unique structure. An isotopologue is usually comprised of a family of isotopic isomers (isotopomers) which differ by the location of the isotopes on the molecule (*e.g.*, CH_3NHD and CH_2DNH_2 are the same isotopologue but are different isotopomers).

"Isotopic content" refers to the content of isotopes in a molecule or population of molecules relative to the content in the molecule or population of molecules naturally (*i.e.*, prior to administration or contacting of isotope labeled precursor molecules). The term "isotope enrichment" is used interchangeably with isotopic content herein.

"Isotopic pattern" refers to the internal relationships of isotopic labels within a molecule or population of molecules, *e.g.*, the relative proportions of molecular species with different isotopic content, the relative proportions of molecules with isotopic labels in different chemical

loci within the molecular structure, or other aspects of the internal pattern rather than absolute content of isotopes in the molecule.

"Exact mass" refers to mass calculated by summing the exact masses of all the isotopes in the formula of a molecule (e.g., 32.04847 for CH_3NHD).

"Nominal mass" refers to the integer mass obtained by rounding the exact mass of a molecule.

"Mass isotopomer" refers to family of isotopic isomers that is grouped on the basis of nominal mass rather than isotopic composition. A mass isotopomer may comprise molecules of different isotopic compositions, unlike an isotopologue (*e.g.*, CH_3NHD, $^{13}CH_3NH_2$, $CH_3{}^{15}NH_2$ are part of the same mass isotopomer but are different isotopologues). In operational terms, a mass isotopomer is a family of isotopologues that are not resolved by a mass spectrometer. For quadrupole mass spectrometers, this typically means that mass isotopomers are families of isotopologues that share a nominal mass. Thus, the isotopologues CH_3NH_2 and CH_3NHD differ in nominal mass and are distinguished as being different mass isotopomers, but the isotopologues CH_3NHD, CH_2DNH_2, $^{13}CH_3NH_2$, and $CH_3{}^{15}NH_2$ are all of the same nominal mass and hence are the same mass isotopomers. Each mass isotopomer is therefore typically composed of more than one isotopologue and has more than one exact mass. The distinction between isotopologues and mass isotopomers is useful in practice because all individual isotopologues are not resolved using quadrupole mass spectrometers and may not be resolved even using mass spectrometers that produce higher mass resolution, so that calculations from mass spectrometric data must be performed on the abundances of mass isotopomers rather than isotopologues. The mass isotopomer lowest in mass is represented as M_0; for most organic molecules, this is the species containing all ^{12}C, ^{1}H, ^{16}O, ^{14}N, etc. Other mass isotopomers are distinguished by their mass differences from M_0 (M1, M2, etc.). For a given mass isotopomer, the location or position of isotopes within the molecule is not specified and may vary (i.e., "positional isotopomers" are not distinguished).

"Mass isotopomer envelope" refers to the set of mass isotopomers comprising the family associated with each molecule or ion fragment monitored.

"Mass isotopomer pattern" refers to a histogram of the abundances of the mass isotopomers of a molecule. Traditionally, the pattern is presented as percent relative abundances where all of the abundances are normalized to that of the most abundant mass isotopomer; the most abundant isotopomer is said to be 100%. The preferred form for applications involving probability analysis, such as mass isotopomer distribution analysis (MIDA), however, is proportion or fractional abundance, where the fraction that each species contributes to the total abundance is used. The term "isotope pattern" may be used synonymously with the term "mass isotopomer pattern."

"Monoisotopic mass" refers to the exact mass of the molecular species that contains all ^{1}H, ^{12}C, ^{14}N, ^{16}O, ^{32}S, etc. For isotopologues composed of C, H, N, O, P, S, F, Cl, Br, and I, the isotopic composition of the isotopologue with the lowest mass is unique and unambiguous because the most abundant isotopes of these elements are also the lowest in mass. The monoisotopic mass is abbreviated as m0 and the masses of other mass isotopomers are identified by their mass differences from m0 (m1, m2, etc.).

"Isotopically perturbed" refers to the state of an element or molecule that results from the explicit incorporation of an element or molecule with a distribution of isotopes that differs from the distribution that is most commonly found in nature, whether a naturally less abundant isotope is present in excess (enriched) or in deficit (depleted).

"Precursor molecule" refers to the metabolic precursors used during polymeric synthesis of specific molecules. Examples of precursor molecules include acetyl CoA, ribonucleic acids, deoxyribonucleic acids, amino acids, glucose, and glycine.

"Labeled water" as used herein refers to water that contains isotopes. Examples of labeled water include $^{2}H_2O$, $^{3}H_2O$, and $H_2{}^{18}O$. As used herein, the term "isotopically labeled water" is used interchangeably with "labeled water."

"Molecular flux rates" refers to the rate of synthesis and/or breakdown of molecules within a cell, tissue, or organism. "Molecular flux rates" also refers to a molecule's input into or removal from a pool of molecules, and is therefore synonymous with the flow into and out of said pool of molecules.

"Drug agent, " "pharmaceutical agent," and "pharmacological agent" are used interchangeably and refer to chemical entities or biological agents (*e.g.*, gene sequences, poly or monoclonal antibodies, cytokines, hormones, etc.) with useful or potentially useful therapeutic actions on biological processes that have been used or approved for use or are being tested or considered for use as therapeutic agents in humans or animals. Drug agents include, but are not limited to, any chemical compound or composition disclosed in, for example, the 13th Edition of *The Merck Index* (a U.S. publication, Whitehouse Station, N.J., USA), incorporated herein by reference in its entirety. "Known drugs" refers to agents or chemical entities that have been approved for therapeutic use as drugs in human beings in the United States.

By "molecule of interest" is meant any molecule, including but not limited to, cholesterol, cholesterol derivatives, bile acids, bile acid derivatives, amino acids, carbohydrates, fatty acids, peptides, sugars, lipids, nucleic acids, polynucleotides, glycosaminoglycans, polypeptides, or proteins that are present within a metabolic pathway within a living system.

An "individual" is a vertebrate, preferably a mammal, more preferably a human. The term "subject" is used interchangeably with "individual" herein.

A "biological molecule" refers to any molecule or molecules synthesized in a tissue or individual. A biological may refer to a class of molecules, such as, but not limited to, the set of total cellular proteins, genomic DNA, mitochondrial DNA, messenger RNA, or ribosomal RNA. Alternatively, biological molecules may be specific molecules with specific structural features or sequences, such as specific proteins (for example, apolipoprotein) or specific polynucleotide sequences (for example, a polynucleotide encoding apolipoprotein).

As used herein, an individual "at risk" is an individual who is considered more likely to develop a disease state or a physiological state than an individual who is not at risk. An individual "at risk" may or may not have detectable symptoms indicative of the disease or physiological condition, and may or may not have displayed detectable disease prior to the treatment methods (e.g., therapeutic intervention) described herein. "At risk" denotes that an individual has one or more so-called risk factors. An individual having one or more of these risk factors has a higher probability of developing one or more disease(s) or physiological condition(s) than an individual without these risk factor(s). These risk factors can include, but

are not limited to, history of family members developing one or more diseases, related conditions, or pathologies, history of previous disease, age, sex, race, diet, presence of precursor disease, genetic (i.e., hereditary) considerations, and environmental exposure.

"Purifying" refers to methods of removing one or more components of a mixture of other similar compounds. For example, "purifying a protein or peptide" refers to removing a protein or peptide from one or more proteins or peptides in a mixture of proteins or peptides.

"Isolating" refers to separating one compound from a mixture of compounds. For example, "isolating a protein or peptide" refers to separating one specific protein or peptide from all other proteins or peptides in a mixture of one or more proteins or peptides.

A "biological sample" encompasses any sample obtained from a tissue or individual. The definition encompasses blood and other liquid samples of biological origin, that are accessible from an individual through sampling by minimally invasive or non-invasive approaches (e.g., urine collection, blood drawing, needle aspiration, and other procedures involving minimal risk, discomfort or effort). Biological samples include samples that have been manipulated in any way after their procurement, such as by treatment with reagents, solubilization, or enrichment for certain components, such as proteins or polynucleotides. The term "biological sample" also encompasses a clinical sample such as serum, plasma, other biological fluid, or tissue samples, and also includes cells in culture, cell supernatants and cell lysates.

"Biological fluid" includes but is not limited to urine, blood, interstitial fluid, edema fluid, saliva, lacrimal fluid, inflammatory exudates, synovial fluid, abscess, empyema or other infected fluid, cerebrospinal fluid, sweat, pulmonary secretions (sputum), seminal fluid, feces, bile, intestinal secretions, or other biological fluid.

Methods For Measuring Reverse Cholesterol Transport

The present invention provides methods for determining reverse cholesterol transport (RCT) *in vivo* by measuring the flow of unlabeled cholesterol from tissues into the bloodstream and/or from plasma HDL to bile acids, instead of the flow of labeled cholesterol.

In one aspect, the invention is directed to determining the rate of the first arm of reverse cholesterol transport by administering one or more isotopically labeled isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors to a living system. In a second aspect, the present invention is directed to determining the rate of the second arm of reverse cholesterol transport by determining the rate of the first arm of RCT, and administering one or more isotopically labeled bile acids to determine the molecular flux rate of the conversion of plasma cholesterol to bile acid (second arm of RCT). The methods are generally carried out in mammalian subjects, preferably humans. Mammals include, but are not limited to, primates, farm animals, sport animals, pets such as cats and dogs, guinea pigs, rabbits, mice, and rats.

I. Determining the Rate of the First Arm of Reverse Cholesterol Transport in the Living System

In one aspect, the rate of the first arm of reverse cholesterol transport may be determined in a living system. One or more isotopically labeled isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors are administered to the living system for a period of time sufficient for the label to be incorporated in plasma HDL. One or more isotopically labeled cholesterol molecules are obtained from plasma HDL. The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the cholesterol molecules is then measured. The rate of dilution of the isolated labeled cholesterol molecules by endogenous unlabeled cholesterol is then calculated to determine the rate of the first arm of reverse cholesterol transport in the living system.

A. Administering isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors

Isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors can be administered to a living system by various methods including, but not limited to, orally, parenterally, subcutaneously, intravenously, and intraperitoneally.

Isotopically labeled HDL particles are typically formed *ex vivo* (outside of the subject) for example by incubating apolipoproteinAI with egg phosphatidylcholine, free $^{2}H_{6}$-cholesterol, and cholic acid in the ratio of 1:80:8:80. Other suitable ranges can be determined by trial and

error using procedures well known to those of ordinary skill in the art without undue experimentation. In a preferred embodiment, a plasma fraction or purified enzyme containing lecithin-cholesterol-acyl-transferase activity as well as serum albumin to carry phosphatidylcholine is then added, followed by removal of the enzymes and cholic acid by such techniques as size exclusion chromatography and dialysis, respectively. In general, the reconstituted HDL particles will be formed by mixing. Other methods for forming cholesterol-labeled HDL particles *ex vivo* are well known by or can be readily determined by those skilled in the art.

The HDL particles may be labeled *in vivo* by administering isotopically labeled cholesterol or an isotopically labeled precursor of cholesterol to the subject, followed by obtaining the labeled HDL from plasma. The labeling of cholesterol and cholesterol precursors using isotopes may be carried out by methods well known in the art. Isotopes that may be used for *in vitro* or *in vivo* cholesterol labeling include, but are not limited to ^{2}H, ^{3}H, ^{13}C, ^{14}C, or ^{18}O. Cholesterol molecules suitable for labeling include free cholesterol, cholesterol ethers, and cholesterol esters. In a preferred variation, cholesterol esters are labeled.

The isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors may be continuously or repeatedly administered. Administration can be achieved in various ways. Administration may be accomplished continuously or repeatedly. The isotopically labeled high density lipoprotein (HDL) particles, isotopically labeled cholesterol molecules, or isotopically labeled cholesterol precursors may also be administered discontinuously. For the discontinuous labeling method, administration is accomplished one or more times, and then administration is discontinued and wash-out of labeled administered particle or molecule from body precursor pools is allowed to occur.

The methods of this invention are typically carried out in mammalian subjects, preferably humans. Mammals include, but are not limited to, primates, farm animals, sport animals, mice, and rats.

The isotopically labeled HDL particles, isotopically labeled cholesterol, or isotopically labeled precursors are generally administered in a suitable carrier at a predetermined volume and isotope concentration (to yield a certain specific activity). Suitable carriers include saline

solution, triglyceride emulsions and intralipids. Isotope concentration typically varies depending on the purpose, e.g., if being given as a bolus or as maintenance administration. The isotopically labeled HDL particles, isotopically labeled cholesterol, or isotopically labeled precursors are administered for a length of time sufficient to achieve steady-state levels in the HDL-cholesterolin plasma.

B. Obtaining Isotopically labeled cholesterol from Plasma HDL

After administration of the labeled HDL particles, cholesterol, or cholesterol precursor molecules, a biological sample is obtained. Isotopically labeled cholesterol from the HDL fraction of the biological sample is obtained, partially purified, or isolated by techniques well known in the art.

The frequency of biological sampling can vary depending on different factors. Such factors include, but are not limited to, the nature of the biological sample, ease and safety of sampling, biological rate constants and turnover kinetics of the cholesterol, and the half-life of a drug agent that is administered to a subject or individual.

The labeled cholesterol may also be purified partially purified, or optionally, isolated, by conventional purification methods including high pressure liquid chromatography (HPLC), fast performance liquid chromatography (FPLC), chemical extraction, thin layer chromatography, gas chromatography, gel electrophoresis, and/or other separation methods known to those skilled in the art.

In another embodiment, the isotopically labeled cholesterol may be hydrolyzed or otherwise degraded to form smaller molecules. Hydrolysis methods include any method known in the art, including, but not limited to, chemical hydrolysis (such as acid hydrolysis) and biochemical degradation. Hydrolysis or degradation may be conducted either before or after purification and/or isolation of the cholesterol. The cholesterol also may be partially purified, or optionally, isolated, by conventional purification methods including high performance liquid chromatography (HPLC), fast performance liquid chromatography (FPLC), gas chromatography, gel electrophoresis, and/or any other methods of separating chemical and/or biochemical compounds known to those skilled in the art.

The cholesterol may also be derivatized. For example, the cholesterol may be derivatized to its TMS derivative prior to detection.

Methods of obtaining, purifying, and isolating cholesterol molecules may be found, for example, in Cell Biology: A Laboratory Notebook (J.E. Cellis, ed., 1998); Current Protocols in Molecular Biology (F.M. Ausubel et al., eds, 1987); Short Protocols in Molecular Biology (Wiley and Sons, 1999), as well as other sources well known in the art.

C. Measuring the isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the isotopically labeled cholesterol molecules

The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the isotopically labeled cholesterol molecules is then determined. The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the isotopically labeled cholesterol molecules may be determined by methods including, but not limited to, mass spectrometry, nuclear magnetic resonance (NMR) spectroscopy, liquid scintillation counting or other methods known in the field. The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of cholesterol may be measured directly, or may be analyzed after the cholesterol has been chemically or biochemically modified.

1. Mass Spectrometry

Isotopic enrichment in isotopically labeled cholesterol molecules can be determined by various methods such as mass spectrometry, including but not limited to gas chromatography-mass spectrometry (GC-MS), isotope-ratio mass spectrometry, GC-isotope ratio-combustion-MS, GC-isotope ratio-pyrrolysis-MS, liquid chromatography-MS, electrospray ionization-MS, matrix assisted laser desorption-time of flight-MS, Fourier-transform-ion-cyclotron-resonance-MS, and cycloidal-MS.

Mass spectrometers convert molecules into rapidly moving gaseous ions and separate them on the basis of their mass-to-charge ratios. The distributions of isotopes or isotopologues of ions, or ion fragments, may thus be used to measure the isotopic enrichment in a plurality of molecules.

Generally, mass spectrometers include an ionization means and a mass analyzer. A number of different types of mass analyzers are known in the art. These include, but are not limited to, magnetic sector analyzers, electrospray ionization, quadrupoles, ion traps, time of flight mass analyzers, and Fourier transform analyzers.

Mass spectrometers may also include a number of different ionization methods. These include, but are not limited to, gas phase ionization sources such as electron impact, chemical ionization, and field ionization, as well as desorption sources, such as field desorption, fast atom bombardment, matrix assisted laser desorption/ionization, and surface enhanced laser desorption/ionization.

In addition, two or more mass analyzers may be coupled (MS/MS) first to separate precursor ions, then to separate and measure gas phase fragment ions. These instruments generate an initial series of ionic fragments of a molecule, and then generate secondary fragments of the initial ions. The resulting overlapping sequences allows complete sequencing of the protein, by piecing together overlaying "pieces of the puzzle", based on a single mass spectrometric analysis within a few minutes (plus computer analysis time).

The MS/MS fragmentation patterns and exact molecular mass determinations generated by mass spectrometry provide unique information regarding the chemical composition of molecules. An unknown molecule can be identified in minutes, by a single mass spectrometric analytic run. The library of chemical fragmentation patterns that is now available provides the opportunity to identify components of complex mixtures with near certainty.

Different ionization methods are also known in the art. One key advance has been the development of techniques for ionization of large, non-volatile macromolecules. Techniques of this type have included electrospray ionization (ESI) and matrix assisted laser desorption/ionization (MALDI). These have allowed MS to be applied in combination with powerful sample separation introduction techniques, such as liquid chromatography and capillary zone electrophoresis.

In addition, mass spectrometers may be coupled to separation means such as gas chromatography (GC) and high performance liquid chromatography (HPLC). In gas-chromatography mass-spectrometry (GC/MS), capillary columns from a gas chromatograph are coupled directly to the mass spectrometer, optionally using a jet separator. In such an application, the gas chromatography (GC) column separates sample components from the sample gas mixture and the separated components are ionized and chemically analyzed in the mass spectrometer.

When GC/MS is used to measure mass isotopomer abundances of organic molecules, hydrogen-labeled isotope incorporation from isotope-labeled water is amplified 3 to 7-fold, depending on the number of hydrogen atoms incorporated into the organic molecule.

In general, in order to determine a baseline mass isotopomer frequency distribution for the cholesterol or cholesterol derivative, such a sample is taken before infusion of an isotopically labeled precursor. Such a measurement is one means of establishing in the cell, tissue or organism, the naturally occurring frequency of mass isotopomers of the molecule of interest. When a cell, tissue or organism is part of a population of subjects having similar environmental histories, a population isotopomer frequency distribution may be used for such a background measurement. Additionally, such a baseline isotopomer frequency distribution may be estimated, using known average natural abundances of isotopes. For example, in nature, the natural abundance of ^{13}C present in organic carbon is 1.11%. Methods of determining such isotopomer frequency distributions are discussed below. Typically, samples of the molecule of interest are taken prior to and following administration of an isotopically labeled molecule to the subject and analyzed for isotopomer frequency.

D. Calculating the Rate of Dilution of Isotopically Labeled Cholesterol Molecules

The isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the isotopically labeled cholesterol molecules after administration is compared to the isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the isotopically labeled cholesterol molecules of the HDL particles or cholesterol precursors prior to administration to calculate the dilution of labeled cholesterol by unlabeled cholesterol. Dilution equations are known in the art and are described, for example, by Hellerstein et al. (1992), *supra*. The rate of dilution is then used to determine the molecular flux rate of tissue cholesterol into HDL, which corresponds to the first arm of RCT.

The rate of dilution of plasma cholesterol may be determined directly by subtracting the rate of infusion of unlabeled cholesterol from the rate of infusion of labeled cholesterol.

$$DilutionRate = \frac{InfusionRate(labeledCholesterol)}{Enrichment(LabeledCholesterol)} - InfusionRate(LabeledCholesterol)$$

II. Determining the molecular flux rate of the second arm of reverse cholesterol transport in the living system

In another aspect, the present invention is directed to first determining the rate of the first arm of reverse cholesterol transport, and second determining the rate of the second arm of reverse cholesterol transport.

A. Determining the Rate of the First Arm of RCT

To determine the rate of the second arm of RCT, the rate of the first arm of RCT is determined as described above. The rate of the second arm of reverse cholesterol transport is also determined as described below.

B. Administering One or more Isotopically Labeled Bile Acids

One or more isotopically labeled bile acids are administered to the living system in a manner different than the manner in which the label of the isotopically labeled HDL particle, isotopically labeled cholesterol, or isotopically labeled cholesterol precursor molecule are administered. Alternatively, the isotopically labeled bile acids have a different isotope label than the isotopically labeled HDL particle, isotopically labeled cholesterol, or isotopically labeled cholesterol precursor. One or more isotopically labeled bile acids is obtained from the living system, and the isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of the bile acid is measured. The molecular flux rate of converting plasma HDL-cholesterol to bile acids is calculated to determine the rate of second arm of reverse cholesterol transport in the living system, thereby determining the rate of reverse cholesterol transport in the living system.

Suitable isotopically labeled bile acids include cholic acid, chenodeoxycholic acid, deoxycholic acid, and lithocholic acid. The preferred labeled bile acids are cholic acid and chenodeoxycholic acid. Isotopes that may be used for labeling the bile acids include, but are not limited to, ^{2}H, ^{3}H, ^{13}C, ^{14}C, or ^{18}O.

The bile acids that are administered are labeled with an different isotope label from the isotope label used to label the HDL, cholesterol, or cholesterol precursor. Alternatively, the bile acids are labeled with the same isotope as the HDL, cholesterol, or cholesterol precursor but the bile acids are labeled in a manner that is distinguishable from the manner used to label the

cholesterol or cholesterol precursor (e.g different times, pulse, stopping vs. continuous and other distinguishable features well known to those skilled in the art).

The isotopically labeled bile acids may be administered simultaneously with, or separately from, the isotopically labeled HDL particles, isotopically labeled cholesterol, or isotopically labeled cholesterol precursors. The isotopically labeled bile acids are administered in a suitable carrier at a predetermined volume and isotope concentration (to yield a certain specific activity). Suitable carriers include saline solution, triglyceride emulsions and intralipids. Isotope concentration typically varies depending on the purpose, e.g., if being given as a bolus or as maintenance administration. Like the labeled HDL particles, labeled cholesterol ,or labeled cholesterol precursors, and isotopically labeled bile acids are administered for a duration of time sufficient to achieve steady-state levels in the molecules of interest.

The administration of labeled bile acids to subjects may be orally or by paritoneal routes, e.g., intravascular infusion or subcutaneous, intramuscular, or intraperitoneal injection.

The bile acid may be obtained, and the isotopic content, isotopic pattern, rate of change of isotopic content, or rate of change of isotopic pattern may be calculated, as described for cholesterol, above.

If a labeled bile acid is administered in conjunction with labeled HDL to the subject, labeled cholesterol is obtained from the bile acids in the biological sample by techniques well known in the art. As described herein, the isotopic label of the administered bile acid is distinguishable from that of the administered HDL.

D. Measuring the isotopic content, isotopic pattern, rate of change of isotopic content, or isotopic pattern of isotopically labeled Bile Acids

Isotopic enrichment of the isolated bile acids is then determined from both the administered HDL particles and the administered bile acids, and compared to the isotopic content of the HDL particles and bile acids prior to administration. The contribution from HDL cholesterol to bile acids and the dilution (total flux) of bile acids to labeled cholesterol in bile by unlabeled cholesterol is calculated. In this manner, the rate of the second arm of RCT (HDLc to bile acids; Figure 1) can be calculated.

1. Measuring Relative and Absolute Mass Isotopomer Abundances

Measured mass spectral peak heights, or alternatively, the areas under the peaks, may be expressed as ratios toward the parent (zero mass isotope) isotopomer. It is appreciated that any calculation means which provide relative and absolute values for the abundances of isotopomers in a sample may be used in describing such data, for the purposes of the present invention.

2. Calculating Labeled:Unlabeled Proportion of Molecules of Interest

The proportion of labeled and unlabeled molecules of interest is then calculated. The practitioner first determines measured excess molar ratios for isolated isotopomer species of a molecule. The practitioner then compares measured internal pattern of excess ratios to the theoretical patterns. Such theoretical patterns can be calculated using the binomial or multinomial distribution relationships as described in U.S. Patents Nos. 5,338,686, 5,910,403, and 6,010,846, which are hereby incorporated by reference in their entirety. The calculations may include Mass Isotopomer Distribution Analysis (MIDA). Variations of Mass Isotopomer Distribution Analysis (MIDA) combinatorial algorithm are discussed in a number of different sources known to one skilled in the art. The method is further discussed by Hellerstein and Neese (1999), as well as Chinkes, et al. (1996), and Kelleher and Masterson (1992), and U.S. Patent Application No. 10/279,399, all of which are hereby incorporated by reference in their entirety.

In addition to the above-cited references, calculation software implementing the method is publicly available from Professor Marc Hellerstein, University of California, Berkeley.

The comparison of excess molar ratios to the theoretical patterns can be carried out using a table generated for a molecule of interest, or graphically, using determined relationships. From these comparisons, a value, such as the value p, is determined, which describes the probability of mass isotopic enrichment of a subunit in a precursor subunit pool. This enrichment is then used to determine a value, such as the value A_X^*, which describes the enrichment of newly synthesized molecules for each mass isotopomer, to reveal the isotopomer excess ratio which would be expected to be present, if all isotopomers were newly synthesized.

Fractional abundances are then calculated. Fractional abundances of individual isotopes (for elements) or mass isotopomers (for molecules) are the fraction of the total abundance

represented by that particular isotope or mass isotopomer. This is distinguished from relative abundance, wherein the most abundant species is given the value 100 and all other species are normalized relative to 100 and expressed as percent relative abundance. For a mass isotopomer M_X,

$$Fractional\ abundance\ of\ M_X = A_X = \frac{Abundance\ M_x}{\sum_{i=0}^{n} Abundance\ M_i}$$, where 0 to n is the range of nominal masses relative to the lowest mass ($M0$) mass isotopomer in which abundances occur.

$$\Delta\ Fractional\ abundance\ (enrichment\ or\ depletion) = (A_x)_e - (A_x)_b = \left(\frac{Abundance\ M_x}{\sum_{i=0}^{n} Abundance\ M_i}\right)_e - \left(\frac{Abundance\ M_x}{\sum_{i=0}^{n} Abundance\ M_i}\right)_b,$$

where subscript e refers to enriched and b refers to baseline or natural abundance.

In order to determine the fraction of the molecules that were actually newly synthesized during a period of precursor administration, the measured excess molar ratio (EM_X) is compared to the calculated enrichment value, A_X^*, which describes the enrichment of newly synthesized biopolymers for each mass isotopomer, to reveal the isotopomer excess ratio which would be expected to be present, if all isotopomers were newly synthesized.

E. Calculating the Molecular Flux Rate of Converting HDL Cholesterol to Bile Acid

The method of determining rate of synthesis includes calculating the proportion of mass isotopically labeled subunit present in the molecular precursor pool, and using this proportion to calculate an expected frequency of a molecule of interest containing at least one mass isotopically labeled subunit. This expected frequency is then compared to the actual, experimentally determined isotopomer frequency of the molecule of interest. From these values, the proportion of the molecule of interest which is synthesized from added isotopically labeled

precursors during a selected incorporation period can be determined. Thus, the rate of synthesis during such a time period is also determined.

A precursor-product relationship may then be applied to determine the percentage of labeled bile acid from the isotopically labeled HDL, isotopically labeled cholesterol, or isotopically labeled cholesterol precursor. For the continuous labeling method, the isotopic enrichment is compared to asymptotic (*i.e.*, maximal possible) enrichment and kinetic parameters (*e.g.*, synthesis rates) are calculated from precursor-product equations. The fractional synthesis rate (k_s) may be determined by applying the continuous labeling, precursor-product formula:

$$k_s = [-\ln(1-f)]/t,$$

where f = fractional synthesis = product enrichment/asymptotic precursor/enrichment

and t = time of label administration of contacting in the system studied.

For the discontinuous labeling method, the rate of decline in isotope enrichment is calculated and the kinetic parameters of the molecules of interest are calculated from exponential decay equations. Breakdown rate constants (k_d) may be calculated based on an exponential or other kinetic decay curve:

$$k_d = [-\ln f]/t.$$

The dilution rate of isotopically labeled bile acid may be calculated by equations known in the art such as, for example, the following equation:

$$DilutionRate = \frac{InfusionRate(labeledBileAcid)}{Enrichment(LabeledBileAcid)} - InfusionRate(LabeledBileAcid).$$

The rate of the second arm of RCT may be calculated by multiplying the percent of bile acid from cholesterol with the dilution rate in the living system according to equations known in the art, such as, for example, the following equation:

$$RateofSecondArm = \%BilefromCholesterol \otimes RateofBileTurnover.$$

Uses of Determining the Rate of Reverse Cholesterol Transport (RCT)

The methods of the present invention may be used for a variety of purposes. Primarily, the methods are used to determine the rates of the first and second arms RCT in a subject. In turn, the rates may be used to assess the effect of various factors on atherogenesis.

For example, in one variation, the methods may be used to assess the effect of a drug agent on atherosclerosis. After administering the drug agent to a subject, the rate of the first arm or the second arm RCT in the subject before and after administration of the drug agent will be compared. The subject may or may not have atherosclerosis. The effect of the candidate drug agent will be determined by the change (e.g., increase, decrease, or no difference) in the rate measured before and after administration of the drug agent. The drug agent may be a known pharmaceutical agent or deoxyribonucleic acid molecule that is capable of affecting the first and/or second arm of RCT.

In another variation, the methods may be used to assess the effect of dietary modification on atherosclerosis. Similar to that described above, the effect is determined by the change (e.g., increase, decrease, or no difference) in the rate of first and/or second arm of RCT determined before and after dietary modification.

In a further variation, the invention provides kits for performing the methods of the invention. The kits may be formed to include such components as labeled HDL particles, labeled cholesterol, labeled bile acids, or a combination thereof, in varying isotope concentrations and as premeasured volumes. Furthermore, the kit preferably will be packaged with instructions for use of the kit components and with instructions on how to calculate cholesterol dilutions.

Other kit components, such as tools for administration of the labeled HDL particles, labeled cholesterol, or labeled bile acids (e.g., measuring cup, needles, syringes, pipettes, IV tubing), may optionally be provided in the kit. Similarly, instruments for obtaining samples from the subject (e.g., specimen cups, needles, syringes) may also be optionally provided.

The following example is provided to show that the method of the invention may be used to determine reverse cholesterol transport. Those skilled in the art will recognize that while

specific embodiments have been illustrated and described, they are not intended to limit the invention.

EXAMPLES

Example 1

Measurement of Reverse Cholesterol Transport in an Animal Model

Figure 2 shows an experimental protocol that is used in an experiment involving an animal model, such as a rat model. Infusion catheters are surgically placed in the jugular vein of rats which are then allowed to recover for 24 hours. An IV bolus of [$^2H_4$]-BA and [1-$^{13}C_1$]-acetate is given followed by constant IV infusion of HDL-[$^2H_6$]C-E (cholesterol ester). Blood samples are obtained after 2 hours and at sacrifice 24 hours later. At sacrifice, feces are also collected.

Cholesterol from blood and fecal samples is then obtained. In each sample, the cholesterol is then derivatized to its TMS derivative and measured by mass spectrometry. The rate of the first arm of reverse cholesterol synthesis is calculated.

Example 2

Measuring Reverse Cholesterol Transport in a Murine Model

Figure 2 shows an experimental protocol that is used in an experiment involving an animal model, such as a rat model. Infusion catheters are surgically placed in the jugular vein of rats which are then allowed to recover for 24 hours. An IV bolus of [$^2H_4$]-BA and [1-$^{13}C_1$]-acetate is given followed by constant IV infusion of HDL-[$^2H_6$]C-E (cholesterol ester). Blood samples are obtained after 2 hours and at sacrifice 24 hours later. At sacrifice, feces are also collected.

Cholesterol from blood and fecal samples is then obtained. In each sample, the cholesterol is then derivatized to its TMS derivative and measured by mass spectrometry. The bile acid is also obtained, derivatized, and measured by mass spectrometry. The rate of the first

arm of reverse cholesterol transport is calculated based on the cholesterol measurement. The rate of the second arm of reverse cholesterol is calculated based on the bile acid measurement.

Applicants have not abandoned or dedicated to the public any unclaimed subject matter.